



SEQUENCE LISTING

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<120> CRYSTAL STRUCTURE OF BETA SITE APP CLEAVING ENZYME
(BACE) AND METHODS OF USE THEREOF

<130> 674553-2002.1

<140> 10/627,473
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<150> 60/398,681
<151> 2002-07-26

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<170> PatentIn Ver. 2.1

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Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
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Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
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Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
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 Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
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 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
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 <212> PRT
 <213> Homo sapiens

<400> 10

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Ala
 1 5 10 15

Gly Val Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu
 20 25 30

Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu
 35 40 45

Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Gly Ser Phe Val Glu Met
 50 55 60

Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
 65 70 75 80

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
 85 90 95

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
 100 105 110

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
 115 120 125

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
 130 135 140

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
 145 150 155 160

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
 165 170 175

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
 180 185 190

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val
 195 200 205

Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn
 210 215 220

Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
 225 230 235 240

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
 245 250 255

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
 260 265 270

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
 275 280 285

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
 290 295 300

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
 305 310 315 320

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
 325 330 335

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
 340 345 350

Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
 355 360 365

Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe
 370 375 380

Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met
 385 390 395 400

Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe
 405 410 415

Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val
 420 425 430

Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile
 435 440 445

Pro Gln Thr Asp Glu Ser
 450

<210> 11

<211> 1386

<212> DNA

<213> Homo sapiens

<400> 11

atggctagca tgactggtgg acagcaaattg ggtcgccggat ccatggcgggg agtgctgcct 60
 gcccacggca cccagcacgg catccggctg cccctgcgca gcggcctggg gggcgcccc 120
 ctggggctgc ggctgccccg ggagacccgac gaagagcccg aggagcccg caagaagggc 180
 agctttgtgg agatggtggg caacctgagg ggcaagtctgg ggcagggtcta ctacgtggag 240
 atgaccgtgg gcagcccccc gcagacgctc aacatcttgg tggatcacgg cagcagtaac 300
 tttgcagtgg gtgctgcccc ccaccccttc ctgcatecgct actaccagag gcagctgtcc 360
 agcacatacc gggacctccg gaagggtgtg tatgtccct acaccaggaa caagtgggaa 420
 ggggagctgg gcaccgaccc ggtaagcatc cccatggcc cccaggtcac tttgcgtgcc 480
 aacattgctg ccatcaactga atcagacaag ttcttcattcc agggctccaa ctgggaaggc 540
 atcctggggc tggcctatgc tgagattgcc aggcctgacg actcccttggc gcctttcttt 600
 gactctctgg taaaggcagac ccacgttcccc aacctttct ccctgcagct ttgtgggtgt 660
 ggctttcccc tccagcagtc tgaagtgtcg gcctctgtcg gagggagcat gatcattgga 720
 ggtatcgacc actcgctgtt cacaggcagt ctctggata caccatccg gcccggagttgg 780
 tattatgagg tgatcattgt ggggtggag atcaatggac aggatctgaa aatggactgc 840
 aaggagtaca actatgacaa gacgttgc gacagtggca ccaccaaccc tcgtttgcc 900
 aagaaagtgt ttgaagctgc agtcaaattcc atcaaggcag cctccatccac ggagaagtcc 960
 cctgtatgggt tctggctagg agagcagctg gtgtgttggc aacggcggcac cacccttgg 1020
 aacatttcc cagtcatctc actctaccta atgggtgagg ttacccagca gtccttccgc 1080
 atcaccatcc ttccgcagca atacctgcgg ccagtgaaag atgtggccac gtcccaagac 1140
 gactgttaca agtttgcatt ctcacagtca tccacgggca ctgttatggg agctgttatac 1200
 atggaggggct tctacgttgc ttgtatggc gcccggaaac gaattggctt tgctgtcagc 1260
 gcttggccatg tgcacgtga gttcaggacg gcagcgggtgg aaggccctt tgtcacccctt 1320
 gacatggaaag actgtggcta caacattcca cagacagatg agtcacatca ccatcatcac 1380
 cactaa 1386

<210> 12
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Ala
 1 5 10 15
 Gly Val Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu
 20 25 30
 Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu
 35 40 45
 Thr Asp Glu Glu Pro Glu Glu Pro Gly Lys Lys Gly Ser Phe Val Glu
 50 55 60
 Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 65 70 75 80
 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 85 90 95
 Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 100 105 110
 Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 115 120 125
 Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 130 135 140
 Thr Asp Leu Val Ser Ile Pro His Gly Pro Gln Val Thr Val Arg Ala
 145 150 155 160
 Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Gln Gly Ser
 165 170 175
 Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 180 185 190
 Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 195 200 205
 Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 210 215 220
 Gln Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 225 230 235 240
 Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 245 250 255
 Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 260 265 270

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 275 280 285
 Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 290 295 300
 Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 305 310 315 320
 Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 325 330 335
 Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 340 345 350
 Glu Val Thr Gln Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 355 360 365
 Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 370 375 380
 Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 385 390 395 400
 Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 405 410 415
 Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 420 425 430
 Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 435 440 445
 Ile Pro Gln Thr Asp Glu Ser His His His His His His
 450 455 460

<210> 13
 <211> 1368
 <212> DNA
 <213> Homo sapiens

<400> 13
 atggcttagca tgactggtgg acagcaaatg ggtcgccgat ccatggcggg agtgctgcct 60
 gcccacggca cccagcacgg catccggctg cccctgcgca gcggcctggg gggcgccccc 120
 ctggggctgc ggctgccccg ggagacccgac gaagagcccg aggagcccg caagaagggc 180
 agcttgtgg agatggtgg aAACCTGAGG ggcaagtcgg ggcagggcta ctacgtggag 240
 atgaccgtgg gcagcccccc gcagacgctc aacatcctgg tggatacagg cagcagtaac 300
 tttgcagtgg gtgctgcccc ccacccttc ctgcacatcgct actaccagag gcagctgtcc 360
 agcacatacc gggacctccg gaagggtgtg tatgtgcctt acaccaggg caagtggaa 420
 ggggagctgg gcaccgaccc ggtaagcata ccccatggcc cccaggtcac tttgcgtgcc 480
 aacatgtgtg ccatcaactga atcagacaag ttcttcatcc agggctccaa ctgggaaggc 540
 atccctgggc tggcctatgc tgagattgcc aggcctgacg actccctggc gcctttctt 600
 gactctctgg taaaggcagac ccacgttccc aacctcttc ccctgcagct ttgtgggtgt 660
 ggcttccccc tccagcagtc tgaagtgtcg gcctctgtcg gagggagcat gatcattgg 720
 ggtatcgacc actcgctgtc cacaggcagt ctctggata caccatccg gcgggagtg 780
 tattatgagg tgatcattgt gcgggtggag atcaatggac aggatctgaa aatggactgc 840

aaggagtaca actatgacaa gagcattgtg gacagtggca ccaccaacct tcgtttgc 900
 aagaaaagtgt ttgaagctgc agtcaaatcc atcaaggcag cctcctccac ggagaagttc 960
 cctgatggtt tctggctagg agagcagctg gtgtgctggc aagcaggcac cacccttgg 1020
 aacattttcc cagtcatctc actctaccta atgggtgagg ttacccagca gtccttccgc 1080
 atcaccatcc ttccgcagca atacctgcgg ccagtggaaag atgtggccac gtcccaagac 1140
 gactgttaca agtttgccat ctcacagtca tccacgggca ctgttatggg agctgttatac 1200
 atggaggggct tctacgttgc tttgatcg gcccggaaac gaattggctt tgctgtcagc 1260
 gcttgccatg tgcacgtatga gttcaggacg gcagcgggtgg aaggccctt tgcacaccc 1320
 gacatggaaag actgtggcta caacattcca cagacagatg agtcatag 1368

<210> 14
 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Ala
 1 5 10 15
 Gly Val Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu
 20 25 30
 Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu
 35 40 45
 Thr Asp Glu Glu Pro Glu Glu Pro Gly Lys Lys Gly Ser Phe Val Glu
 50 55 60
 Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 65 70 75 80
 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 85 90 95
 Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 100 105 110
 Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 115 120 125
 Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 130 135 140
 Thr Asp Leu Val Ser Ile Pro His Gly Pro Gln Val Thr Val Arg Ala
 145 150 155 160
 Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Gln Gly Ser
 165 170 175
 Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 180 185 190
 Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 195 200 205

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 210 215 220
 Gln Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 225 230 235 240
 Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 245 250 255
 Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 260 265 270
 Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 275 280 285
 Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 290 295 300
 Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 305 310 315 320
 Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 325 330 335
 Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 340 345 350
 Glu Val Thr Gln Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 355 360 365
 Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 370 375 380
 Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 385 390 395 400
 Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 405 410 415
 Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 420 425 430
 Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 435 440 445
 Ile Pro Gln Thr Asp Glu Ser
 450 455

<210> 15
 <211> 1386
 <212> DNA
 <213> Homo sapiens

<400> 15
 atggctagca tgactgggtgg acagccaaatg ggtcgccggat ccatggcgggg agtgctgcct 60
 gccccacggca cccagcacgg catccggctg cccctgcgca gcggccctggg gggcgccccc 120

ctggggctgc ggctgccccg ggagaccgac gaagagcccg aggagcccg ccggaaggc 180
 agctttgtgg agatggtgg aacactgagg ggcaagtgg ggcaggctg ctacgtggag 240
 atgaccgtgg gcagcccccc gcagacgctc aacatcctgg tggatacagg cagcagtaac 300
 tttcgtgg gtgctgcccc ccaccccttc ctgcacatcgactaccagag gcagctgtcc 360
 agcacatacc gggacctccg gaagggtgtg tatgtgcct acaccaggaa caagtggaa 420
 ggggagctgg gcaccgaccc ggttaacatc cccatggcc cccaggtcac tgcgtgccc 480
 aacattgctg ccatcactga atcagacaag ttcttcatcc agggctccaa ctggaaaggc 540
 atcctggggc tggcctatgc tgagattgcc aggcctgacg actccctggc gccttctt 600
 gactctctgg taaagcagac ccacgttccc aaccttctt ccctgcagct ttgtgggtct 660
 ggcttcccccc tccagcagtc tgaagtgtg gcctctgtcg gagggagcat gatcattgga 720
 ggtatcgacc actcgctgtc cacaggcagt ctctggata caccatccg gggggagttgg 780
 tattatgagg tgatcattgt ggggtggag atcaatggac aggtatgtaa aatggactgc 840
 aaggagtaca actatgacaa ggcattgtg gacagtggca ccaccaaccc tcgtttgccc 900
 aaggaaatgt ttgaagctgc agtcaaatcc atcaaggcag cctctccac ggagaagttc 960
 cctgtatgtt tctggctagg agagcagctg gtgtgtgtgc aagcaggcac cacccttgg 1020
 aacatccc cagtcatctc actctaccta atgggtgggg ttaccagca gtccctccgc 1080
 atcaccatcc ttccgcagca atacctgcgg ccagtggaaat atgtggccac gtcccaagac 1140
 gactgttaca agtttgccat ctcacagtca tccacgggca ctgttatggg agctgttatac 1200
 atggagggtct tctacgttgc ttgtatgtcg gcccggaaac gaattggctt tgctgtcagc 1260
 gcttgcgttgc tgcacgtatga gttcaggacg gcagcgggg aaggccctt tgcacctt 1320
 gacatgaaag actgtggcta caacattcca cagacagatg agtcacatca ccatcatcac 1380
 cactaa 1386

<210> 16
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Ala
 1 5 10 15
 Gly Val Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu
 20 25 30
 Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu
 35 40 45
 Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Lys Gly Ser Phe Val Glu
 50 55 60
 Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 65 70 75 80
 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 85 90 95
 Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 100 105 110
 Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 115 120 125
 Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 130 135 140

Thr Asp Leu Val Ser Ile Pro His Gly Pro Gln Val Thr Val Arg Ala
 145 150 155 160
 Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Gln Gly Ser
 165 170 175
 Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 180 185 190
 Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 195 200 205
 Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 210 215 220
 Gln Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 225 230 235 240
 Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 245 250 255
 Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 260 265 270
 Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 275 280 285
 Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 290 295 300
 Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 305 310 315 320
 Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 325 330 335
 Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 340 345 350
 Glu Val Thr Gln Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 355 360 365
 Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 370 375 380
 Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 385 390 395 400
 Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 405 410 415
 Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 420 425 430
 Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 435 440 445

Ile Pro Gln Thr Asp Glu Ser His His His His His His His
 450 455 460

<210> 17

<211> 1383

<212> DNA

<213> Homo sapiens

<400> 17

atggctagca tgactgggtgg acagcaaattt ggtcgccggat ccatggccggg agtgctgcct 60
 gcccacggca cccagcacgg catccggctg cccctgcgca gcggcctggg gggcgcccc 120
 ctggggctgc ggctgccccg ggagaccgac gaagagcccg aggagcccg cagggccggc 180
 tttgtggaga tggtgacaa cctgaggggc aagtccgggc agggctacta cgtggagatg 240
 accgtgggca gccccccgca gacgctcaac atccctgggtgg atacaggcag cgttaactt 300
 gcagtggtg ctgccccca ccccttcctg catcgctact accagaggca gctgtccagg 360
 acataccggg acctccggaa gggtgtgtat gtgccttaca cccagggcaa gtgggaaggg 420
 gagctggca ccgacactgtt aagcatcccc catggccccc aggtcactgt gcgtgcac 480
 attgtgccttca tcaactgaatc agacaagttt ttcatccagg gtccttactg ggaaggcatc 540
 ctggggctgg cctatgttgc gattgccagg cctgacact ccctggagcc tttcttgc 600
 tctctggtaa agcagaccca cggtcccaac ctcttctccc tgcagctttg tgggtctggc 660
 ttccccctcc agcagtcttgc agtgcgtggcc tctgtcgagg ggagcatgtat cattggaggt 720
 atcgaccact cgctgtacac aggcagtctc tggatacac ccattccggcg ggagtggat 780
 tatgaggtga tcattgttgc ggtggagatc aatggacagg atctgaaaat ggactgcaag 840
 gagtacaact atgacaagag cattgtggac agtggcacca ccaaccttcg tttgccc 900
 aaagtgtttt aagctgcagt caaatccatc aaggcagctt cctccacggaa gaagttccct 960
 gatggtttctt gcttaggaga gcagctgggtg tgctggcaag caggaccac cccttggaa 1020
 atttttccatc tcatcttactt ctacctaattt ggtggaggtt cccagcagtc ttccgcac 1080
 accatcccttc cgcagcaata cctgccccca gtggaaagatg tggccacgtc ccaagacgac 1140
 ttttacaatgttgc acgttgcactt acggggactgt ttatgggagc ttttatcatg 1200
 gagggcttctt acgttgcactt tgatccggcc cgaaaacgaa ttggcttgc ttttgc 1260
 tgccatgtgc acgttgcactt caggacggca gcgggtggaa gcccctttgt caccctggac 1320
 atggaaagact gtggctacaa cattccacag acagatgagt cacatcacca tcatcaccac 1380
 taa 1383

<210> 18

<211> 460

<212> PRT

<213> Homo sapiens

<400> 18

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Ala
 1 5 10 15

Gly Val Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu
 20 25 30

Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu
 35 40 45

Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Gly Ser Phe Val Glu Met
 50 55 60

Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
 65 70 75 80

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
 85 90 95

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
 100 105 110

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
 115 120 125

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
 130 135 140

Asp Leu Val Ser Ile Pro His Gly Pro Gln Val Thr Val Arg Ala Asn
 145 150 155 160

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Gln Gly Ser Asn
 165 170 175

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
 180 185 190

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val
 195 200 205

Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Gln
 210 215 220

Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
 225 230 235 240

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
 245 250 255

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
 260 265 270

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
 275 280 285

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
 290 295 300

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
 305 310 315 320

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
 325 330 335

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
 340 345 350

Val Thr Gln Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
 355 360 365

Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe
 370 375 380

Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met
 385 390 395 400
 Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe
 405 410 415
 Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val
 420 425 430
 Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile
 435 440 445
 Pro Gln Thr Asp Glu Ser His His His His His His His
 450 455 460

<210> 19
 <211> 411
 <212> PRT
 <213> Homo sapiens

<400> 19
 Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Lys Lys Gly
 1 5 10 15
 Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly
 20 25 30
 Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile
 35 40 45
 Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His
 50 55 60
 Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg
 65 70 75 80
 Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu
 85 90 95
 Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val
 100 105 110
 Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe
 115 120 125
 Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu
 130 135 140
 Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val
 145 150 155 160
 Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala
 165 170 175
 Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser
 180 185 190

Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp
 195 200 205

Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg
 210 215 220

Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn
 225 230 235 240

Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro
 245 250 255

Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser
 260 265 270

Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys
 275 280 285

Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu
 290 295 300

Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu
 305 310 315 320

Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp
 325 330 335

Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met
 340 345 350

Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
 355 360 365

Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
 370 375 380

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
 385 390 395 400

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 405 410

<210> 20
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 <213> Homo sapiens

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Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly
 20 25 30

Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile
 35 40 45

Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His
 50 55 60

Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg
 65 70 75 80

Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu
 85 90 95

Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Gln Val
 100 105 110

Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe
 115 120 125

Ile Gln Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu
 130 135 140

Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val
 145 150 155 160

Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala
 165 170 175

Gly Phe Pro Leu Gln Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser
 180 185 190

Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp
 195 200 205

Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg
 210 215 220

Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn
 225 230 235 240

Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro
 245 250 255

Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser
 260 265 270

Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys
 275 280 285

Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu
 290 295 300

Tyr Leu Met Gly Glu Val Thr Gln Gln Ser Phe Arg Ile Thr Ile Leu
 305 310 315 320

Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp
 325 330 335

Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met
 340 345 350

Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
 355 360 365

Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
 370 375 380

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
 385 390 395 400

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 405 410

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Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly
 20 25 30

Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile
 35 40 45

Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His
 50 55 60

Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg
 65 70 75 80

Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu
 85 90 95

Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Gln Val
 100 105 110

Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe
 115 120 125

Ile Gln Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu
 130 135 140

Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val
 145 150 155 160

Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala
 165 170 175

Gly Phe Pro Leu Gln Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser
 180 185 190

Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp
 195 200 205
 Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg
 210 215 220
 Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn
 225 230 235 240
 Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro
 245 250 255
 Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser
 260 265 270
 Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys
 275 280 285
 Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu
 290 295 300
 Tyr Leu Met Gly Glu Val Thr Gln Gln Ser Phe Arg Ile Thr Ile Leu
 305 310 315 320
 Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp
 325 330 335
 Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met
 340 345 350
 Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
 355 360 365
 Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
 370 375 380
 Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
 385 390 395 400
 Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His His
 405 410 415
 His

<210> 22
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
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<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
ccacaggtgc catctgtgtc tcc 23

<210> 24
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 24
caccagcacc acccagactt gg 22

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
aaccacggag gtgtggtcca gg 22

<210> 26
<211> 39
<212> DNA
<213> Homo sapiens

<400> 26
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<210> 27
<211> 39
<212> DNA
<213> Homo sapiens

<400> 27
catctccaca aagctgccct tcttgcggg ctcctcggg 39

<210> 28

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<211> 40
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<400> 28
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<210> 29
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<400> 29
ccatctccac aaagctgccc ttccggccgg gtcctcggg 40

<210> 30
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<212> DNA
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<400> 30
cccgaggagc ccggcagggg cagcttgtg gagatggtgg ac 42

<210> 31
<211> 42
<212> DNA
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<400> 31
gtccaccatc tccacaaagc tgccctgcc gggctcctcg gg 42

<210> 32
<211> 39
<212> DNA
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<400> 32
cccgaggagc ccggcaagaa gggcagctt gtggagatg 39

<210> 33
<211> 39
<212> DNA
<213> Homo sapiens

<400> 33
catctccaca aagctgccct tcttgcggg ctcctcggg 39

<210> 34
<211> 40
<212> DNA
<213> Homo sapiens

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<400> 34		
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<210> 35		
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<213> Homo sapiens		
<400> 35		
ccatctccac aaagctgccc ttccggccgg gtcctcgaaa		40
<210> 36		
<211> 42		
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gtccaccatc tccacaaaagc tgccctgcc gggctcctcg gg		42
<210> 38		
<211> 39		
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<400> 38		
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<210> 39		
<211> 39		
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<213> Homo sapiens		
<400> 39		
catctccaca aagctgccct tcttggggg ctcctcgaaa		39
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<400> 40		
ccacagacag atgagtcatg acaccatcat caccactaag		40

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<210> 41
<211> 40
<212> DNA
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<400> 41
cttagtggtg atgatggtgt catgactcat ctgtctgtgg 40

<210> 42
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

<400> 42
His His His His His His
1 5

<210> 43
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 43
cgggatccat ggcggggagtg ctgcctgcc 29

<210> 44
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 44
cgggatccctt atgactcatc tgtctgtgga atgttgttagc 40

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His tag
oligonucleotide sequence
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<400> 45
catcaccatc atcaccac

18

<210> 46
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
synthetic fluorescent peptide

<400> 46
Arg Glu Glu Val Asn Leu Asp Ala Glu Phe Lys Arg
1 5 10